

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2000, 14:06:02 ; Search time 9.88 Seconds

(without alignments)
507.675 Million cell updates/sec

Title: US-09-373-230-2

Perfect score: 808

Sequence: 1 NFGRLHCTAVIRININDQV.....KKDENGDKSVNFTLTNLHOS 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	806	99.8	192	1	IL18_MOUSE
2	736.5	91.2	194	1	IL18_RAT
3	538	66.6	193	1	IL18_HORSE
4	518	64.1	193	1	IL18_HUMAN
5	510	63.1	193	1	IL18_CANFA
6	509	63.0	192	1	IL18_PIG
7	82.5	10.2	803	1	IL18_HAEIN
8	82	10.1	267	1	IL18_PIG
9	79.5	9.8	526	1	ZABA_YEAST
10	79	9.8	266	1	IL18_BOVIN
11	78	9.7	1196	1	IL18_BOVIN
12	77	9.5	885	1	BXCN_MOUSE
13	76.5	9.5	167	1	Y809_METUA
14	76.5	9.5	621	1	H7PG_HELPI
15	76.5	9.5	706	1	YK70_YEAST
16	76	9.4	269	1	IL18_MACMU
17	76	9.4	269	1	IL18_MACNE
18	75.5	9.3	270	1	IL18_MOUSE
19	75.5	9.3	439	1	Y811_METUA
20	75.5	9.3	695	1	PGC_HAEIN
21	75	9.3	266	1	IL18_SHEEP
22	75	9.3	268	1	IL18_MACFA
23	75	9.3	624	1	YBY3_SCHPO
24	74.5	9.2	270	1	IL18_PIG
25	74	9.2	269	1	IL18_HUMAN
26	74	9.2	1139	1	RBL2_HUMAN
27	73.5	9.1	589	1	TREG_HHEKA
28	73	9.0	611	1	HBS1_YEAST
29	73	9.0	872	1	VZ2_ROTIC
30	72.5	9.0	698	1	YB06_YEAST
31	72.5	9.0	1010	1	WNT5_DROME
32	72	8.9	207	1	ATPF_MPCPN
33	72	8.9	266	1	IL1B_CEREL

34	71.5	8.8	279	1	ATND_CAVPO
35	71.5	8.8	1215	1	ATC6_YEAST
36	71	8.8	165	1	HSCB_BUCAP
37	71	8.8	541	1	601M_HAEIN
38	71	8.8	628	1	MSLN_HUMAN
39	71	8.8	1547	1	TOP2_BOMMO
40	70.5	8.7	688	1	EPG_MYCPN
41	70.5	8.7	781	1	YB68_SCHPO
42	70	8.7	270	1	IL1A_FELCA
43	70	8.7	527	1	RAG2_MOUSE
44	70	8.7	747	1	AMD1_RAT
45	70	8.7	1381	1	YB67_YEAST

ALIGNMENTS

RESULT	ID	IL18_MOUSE	STANDARD	PRT	192 AA.
1	IL18_MOUSE				
AC	P70380				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)				
DE	(IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).				
GN	IL18 OR IGIF.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.				
RC	TISSUE=LIVER.				
RA	MEDLINE: 96061009.				
RA	Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,				
RA	Tanimoto T., Toriige K., Okura T., Nukada Y., Hattori K.,				
RA	Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.,				
RT	"Cloning of a new cytokine that induces IFN-gamma production by T				
RT	cells."				
RL	Nature 378:88-91(1995).				
RN	[2]				
RP	SEQUENCE OF 1-191 FROM N.A.				
RC	STRAIN=NOB; TISSUE=PANCREAS;				
RA	MEDLINE: 97174346.				
RA	Rothe H., Jenkins N.A., Copeland N.G., Kolb H.,				
RT	"Active stage of autoimmune diabetes is associated with the				
RT	expression of a novel cytokine, IGIF, which is located near idd2."				
RL	J. Clin. Invest. 99:469-474(1997).				
CC	1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS				
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1				
CC	CELLS.				
CC	1- SUBCELLULAR LOCATION: SECRETED.				
CC	1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: D49949; BAA08705.1; -				
DR	EMBL: U66244; AAB49753.1; -				
DR	MGI: MGI:107936; IL18.				
KW	Cytokine.				
FT	PROPEP				
FT	CHAIN				
FT	CONFICT				
FT	SEQUENCE				
SO	192 AA; 22135 MW; 8FED938473874D63 CRC64;				

Query Match

99.8%; Score 806; DB 1; Length 192;

Best Local Similarity 99.4%; Pred. No. 7,1e-67;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 60
DB HFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 95
QY 36 NFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 95
DB 61 VTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYEG 120
QY 96 VTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYEG 155
DB 121 HFLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 157
QY 156 HFLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 192

RESULT 2

IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; P97637; 088749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY; TISSUE-ADRENAL GLAND;
RX MEDLINE; 97152963.
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
cortex";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA";
RL Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DB EMBL: U77776; AAC53009.1; -;
DR EMBL: U77777; AAC53010.1; -;
DR EMBL: AJ22813; CA11001.1; -;
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOPFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 91.2%; Score 736.5; DB 1; Length 194;
Best Local Similarity 89.9%; Pred. No. 1.6e-60;
Matches 142; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

QY 1 NFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 59
DB HFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 96
QY 60 AVTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYE 119
DB 97 AVTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYE 156
QY 120 GHLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 157
DB 157 GHLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 194

RESULT 3

IL18_HORSE STANDARD; PRT; 193 AA.
AC Q9XSQ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Peña-Gonzales M.N., Keanle J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs";
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DB EMBL: Y1131; CAA72013.1; -;
DR EMBL: Y1131; CAA72013.1; -;
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E904ECAF CRC64;

Query Match 66.6%; Score 538; DB 1; Length 193;
Best Local Similarity 68.8%; Pred. No. 2.1e-42;
Matches 106; Conservative 23; Mismatches 42; Indels 2; Gaps 2;

QY 2 NFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 60
DB HFGRLHCTTAVIRININDOVLFDVKRQVPEEDMTIDOSASEPQRLTIYMYKDSVGRGL 97
QY 61 VTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYE 119
DB 98 VTLASVDSKXSTLCKNNKIIISFEEMDPENIDDIOSDILFFQKRVPGHNMKEFESSLYE 157
QY 120 GHLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 153
DB 158 GHLACQKEDDAFKLILKKKDKSGSVMTLTNLHOS 191

RESULT 4
IL18_HUMAN STANDARD; PRT; 193 AA.
ID IL18_HUMAN

RA Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muneta Y., Mori Y.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 DR EMBL: 068701; AAC18415.1; -
 DR EMBL: AB010003; BAA24135.1; -
 KM Cycloline.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 FT SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;
 SQ
 Query Match 63.0%; Score 509; DB 1; Length 192;
 Best Local Similarity 64.9%; Pred. No. 9.1e-40;
 Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
 QY 2 FGRHCTAVIRNINDVLFYDKR-ROPEFEDMDIDQSASPORRLITYWKDSEVNGLA 60
 Db 37 FGRLEPKLSTIRNLNDVLFYDKR-ROPEFEDMDIDQSASPORRLITYWKDSEVNGLA 96
 QY 61 VLSVKDSKSTLSCKNKLIISFEEMDPENIDIDQSLIFEFQKRVPGH-NKMEFESSLYE 119
 Db 97 VLSVQCKKSTLSCKNKLTSEKMSPPDNIDEGNDIIFQKRVPGHDKIQESSLTK 156
 QY 120 GHFLAQEKDDAFKLLKKKDEGDSKSVFTLNLN 153
 Db 157 GYFLACKKENDLFLKLLKEKDEGDSKSVFTLNLN 190
 RESULT 7
 LON_HAEIN STANDARD; PRT; 803 AA.
 AC P43864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ATP-DEPENDENT PROTEASE LA (EC 3.4.21.35).
 GN LON OR LON-A OR HI0462.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=RD / KW20;
 RX MEDLINE: 95350630.
 RA Keriavane A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).

CC -1- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
 CC IN PRESENCE OF ATP. DEGRADATES THE REGULATORY PROTEINS RCSA AND
 CC SULA. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
 CC PROTEIN SUBSTRATE (BY SIMILARITY).
 CC CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
 CC CASEIN AND DENATURATED SERUM ALBUMIN. IN PRESENCE OF ATP.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
 CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
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 CC -----
 DR EMBL: U32729; AAC22121.1; -
 DR TIGR: H10462; -
 DR INTERPRO: IPR001939; -
 DR INTERPRO: IPR001984; -
 DR PFAM: PF00004; AAA; 1.
 DR PRINTS: PR00830; ENDOLAPTASE.
 DR PROSITE: PS01046; LON_SER; 1.
 KM Hydrolyase; Serine protease; ATP-binding.
 FT NP_BIND 356 363 ATP (POTENTIAL).
 FT ACT_SITE 679 679 BY SIMILARITY.
 FT SEQUENCE 803 AA; 89347 MW; 9E590852611EEA5B CRC64;
 SQ

Query Match 10.2%; Score 82.5; DB 1; Length 803;
 Best Local Similarity 18.9%; Pred. No. 4.3;
 Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;
 QY 3 GRHCTAVIRNIND--OVLVFKR-----OPVFEDMDIDQSAS----- 40
 Db 30 GRKKSINALEEAMNDKQILLYSQRADLEFPPEPDLVGTIANIQLKLPDPTVYL 89
 QY 41 -EPQRLIIYWKDSF-----VRGLAVTVLSVKDSKSTLSCKNKLIISFE 83
 Db 90 VEGQNNAKINSLEDKSCSAQITPIETTYGDEKELVAKSAVSEFENYLLNNKVP7D 149
 QY 84 EMDPENIDIT-----OSDLIFQK 103
 Db 150 ILNALQRIDVDRLADTMAHLPSIRKQNALELANVOERLEYLLGMSEADITLQVER 209
 QY 104 RYDGHNMKEFESSIYEGHFLAQKDDAFKLLKKKDEGDSKSVFTLNLHQ 156
 Db 210 RIRGRVKKQKMS-QRNYL-----NEQIKAIRKEMDGENEDTIDEVQLHQ 256
 RESULT 8
 IL1B_PIG STANDARD; PRT; 267 AA.
 AC P26889;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS Sus scrofa (Pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93314975.
 RA Huebner M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
 RT "Cloning, sequencing and regulation of an mRNA encoding porcine
 RT interleukin-1 beta.";
 RL Gene 129:285-289(1993).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
 CC MATURATION & PROLIFERATION. & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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 CC -----
 CC EMBL: M6725; AAA02584.1; -.
 CC PIR: JN0724; JN0724.
 CC HSP: P01584; I1IB.
 CC INTERPRO: IPR000975; -.
 CC INTERPRO: IPR002348; -.
 CC PFAM: PF00340; Interleukin-1; 1.
 CC PRINTS: PR00262; IL1HGF.
 CC PRINTS: PR00264; INTERLEUKIN1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC CYTOKINE; Macrophage; M1ogen; Inflammatory response; Pyrogen.
 CC FT PROPEP 1 114 BY SIMILARITY.
 CC CHAIN 115 267 INTERLEUKIN-1 BETA.
 CC SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;
 SO
 Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 1.3; Indels 12; Gaps 5;
 Matches 23; Conservative 22; Mismatches 31; Indels 12; Gaps 5;
 QY 49 YMKRSEVGLAVTLVSVDKSKTSLCKNK-----IISFENDP---PENIDDIQSLDIF 101
 DB 160 FVGGDDSNKRPVLTGIR-GANLYLSCVMKDNPTPTQLDIDDPKRYFKR--DKERREYVY 216
 QY 102 QKRVPGHNMKEFESSLYEGHFLACQKED 129
 DB 217 KTEI--KNRFEFSALYPNWTYSQAE 242
 RESULT 9
 ZABA_YEAST STANDARD; PRT; 526 AA.
 ID ZABA_YEAST
 AC 000362;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROTEIN PHOSPHATASE PP2A REGULATOR SUBUNIT B (PP25) (CELL DIVISION
 DE CONTROL PROTEIN 55)
 GN CDC55 OR YGL190C OR G1345.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92017858.
 RA Healy A.M., Zolnierowicz S., Stapleton A.E., Goebel M.,
 RA Depaulis-Roach A.A., Pringle J.R.;
 RT CDC55, a Saccharomyces cerevisiae gene involved in cellular
 RT morphogenesis: identification, characterization, and homology to the
 RT B subunit of mammalian type 2A protein phosphatase.*;
 RL Mol. Cell. Biol. 11:5767-5780(1991).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-S288C /FYL1679;
 RX MEDLINE: 97197971.
 RA Coglievina M., Klima R., Bertani I., Delneri D., Zaccaria P.,
 RA Brusch C.V.;
 RT Sequencing of a 40.5 kb fragment located on the left arm of
 RT chromosome VII from Saccharomyces cerevisiae.*;
 RL Yeast 13:55-64(1997).
 CC -1- FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
 CC IN THE CELL SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
 CC CELLULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
 CC CRITICAL SUBSTRATES FOR THIS PHOSPHATASE. THE REGULATORY SUBUNIT
 CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBERT OVERLAPPING,
 CC SUBSETS OF SUBSTRATES.
 CC -1- SUBUNIT: PP2A EXISTS IN SEVERAL TETRAMERIC FORMS, ALL OF WHICH
 CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
 CC A 65 KDA (PP25) (SUBUNIT A) AND A 55 KDA (PP25) (SUBUNIT B)
 CC REGULATORY SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M72716; AAA34482.1; -.
 CC EMBL: 272712; CAA6902.1; -.
 CC EMBL: X91837; CAA62954.1; -.
 CC EMBL: X91489; CAA62785.1; -.
 CC PIR: A41698; A41698.
 CC SGD: S0003158; CDC55.
 CC INTERPRO: IPR000009; -.
 CC PFAM: PF01240; PP25_1.
 CC PRINTS: PR00600; PP2APR55.
 CC PROSITE: PS01024; PP25_1; 1.
 CC PROSITE: PS01025; PP25_2; 1.
 CC Cell cycle.
 CC FT DOMAIN 416 419 POLY-SER.
 CC CONFLICT 500 500 I->N (IN REF. 1).
 CC SEQUENCE 526 AA; 59662 MW; 6DA12C2805FA6AB2 CRC64;
 SO
 Query Match 9.8%; Score 79.5; DB 1; Length 526;
 Best Local Similarity 25.0%; Pred. No. 4.9; Indels 23; Gaps 7;
 Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;
 QY 14 NINDOVL-FVDRKQPVFEDMTDIOASSEFORRLIYMKSEVGLAVTLVSVDKSKST 72
 DB 213 DIPQSFNIVIDIKPTNMELEVTSAEPHPCNLFMYSSSK-----GTRKLDWRQNS 267
 QY 73 LSKNKLISFEEMDPENIDDIQSLDIFPKQKRVPGHNMKEFESSLYEGHFLACQKDDAF 132
 DB 268 L-CDNKTKTFEEYLDPIHNN-----FFTEITSSIDIKRSPN---GRYIASRD----- 311
 QY 133 KLILKKDKNGSKSYMFLITNLRD 156
 DB 312 YLVTKIWDVNMKNPLKTI-NIHE 334
 RESULT 10
 IL1B_BOVIN STANDARD; PRT; 266 AA.
 ID IL1B_BOVIN
 AC P09428;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS Bos taurus (Bovine).
 RN

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89016591.
 RA Leong S.R., Flaeggs G.M., Lawman M., Gray P.W.;
 RA "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
 RL Nucleic Acids Res. 16:9054-9054(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88318652.
 RA Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
 RA Gillis S., Cerretti D.P.;
 RA "Cloning, sequence and expression of bovine interleukin 1 alpha and
 RT interleukin 1 beta complementary DNAs.";
 RL Mol. Immunol. 25:429-437(1988).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M35589; AAA30585.1; -;
 CC DR EMBL: X12498; CAA31018.1; -;
 CC DR EMBL: M37211; AAA30584.1; -;
 CC DR PIR: J10010; ICBO1B.
 CC DR PIR: S01380; S01380.
 CC DR HSSP: P01584; IHB.
 CC DR INTERPRO: IPR000975; -;
 CC DR INTERPRO: IPR002348; -;
 CC DR PIR: PF00340; Interleukin-1; 1.
 CC DR PRINTS: PR00262; IL1HGF.
 CC DR PRINTS: PR00264; INTERLEUKIN1.
 CC DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 CC FT PROPEP 1 113
 CC FT CHAIN 114 266 INTERLEUKIN-1 BETA.
 CC FT CONFLICT 252 252 A -> G (IN REF. 2).
 CC FT SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;

Query Match 9.8%; Score 79; DB 1; Length 266;
 Best Local Similarity 27.5%; Pred. No. 2.4;
 Matches 33; Conservative 18; Mismatches 33; Indels 36; Gaps 8;

QY 40 SEPTRLIIVYWKSEVARG-----LAVTSLVKDSKSTLSCKKK-----IISFEEDMP-- 87
 DB 146 SQEMNREVYVFCM--SFVQGEERDKIKPALGAIKD-KNLYLSCVKKGDTPLTQLEEDVPKV 202
 QY 88 -PENIDDIQSLIFQKRVPGHNMKEFESSLYE-----GHFLACQKEDD 130
 DB 203 YPKR--NMKRFVFKTEI--KNTVEFESVLYPMWYISTQIEERPVLGLHFRAGQDITD 258

RESULT 11

BXCN_CLOBO
 ID BXCN_CLOBO STANDARD; PRT: 1196 AA.
 AC P46081;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE BOTULINUM NEUROTOXIN type C1, NONTOXIC COMPONENT.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TYPE C STOCKHOLM / C-ST;
 RX MEDLINE: 92231894.
 RA Tsuzuki K., Kimura K., Fujii N., Yokosawa N., Oguma K.;
 RA "The complete nucleotide sequence of the gene coding for the
 RT nontoxic-nonhemagglutinin component of Clostridium botulinum type C
 RT progenitor toxin.";
 RL Biochem. Biophys. Res. Commun. 183:1273-1279(1992).
 CC -1- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
 CC TOXICITY.
 CC -----
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 CC -----
 CC DR EMBL: X62389; CAA44262.1; -;
 CC DR INTERPRO: IPR000395; -;
 CC DR PIR: PF01742; Peptidase_M27; 1.
 CC DR PRINTS: PR00760; BONTOTOXINTSIN.
 CC KW Neurotoxin.
 CC SEQUENCE 1196 AA; 138740 MW; 4BD5956274D7F9C3 CRC64;

Query Match 9.7%; Score 78; DB 1; Length 1196;
 Best Local Similarity 24.3%; Pred. No. 18;
 Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;

QY 35 IDQASSEPOTRLIIVYWKSEVGLAV--TLVSKDSKSTLSCKKKIIFSEEDMP-- 90
 DB 965 ISISVDRKQDLIFR-NDKNVANVSIDQILSYISNIISLVKKNSTIYEELSVLDNPI 1023
 QY 91 -----IDDIOSDLIFQKRVPGHNMKEFESSLYEGHFLACQKEDDAEK 133
 DB 1024 TSEVIRNYSYLDNSYIRDSKSLLEYKNKQLYNYVPEPESLYE-----VNDNKKSY 1077
 QY 134 LIKKKDENGDKSVFTLNLAHS 157
 DB 1078 LSLKNTDGINISSVKKFLINIDES 1101

RESULT 12
 UE3A_MOUSE
 ID UE3A_MOUSE STANDARD; PRT: 885 AA.
 AC Q08759; P97482;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE UBIQUITIN-PROTEIN LIGASE E3A (DC 6.3.2.*) (ONCOGENIC PROTEIN-
 DE ASSOCIATED PROTEIN E6-AP).
 GN UE3A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA;
 RX MEDLINE: 97326076.
 RA Hatakeyama S., Jensen J.P., Weissman A.M.;

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RT *Subcellular localization and ubiquitin-conjugating enzyme (E2)
RT interactions of mammalian HECT family ubiquitin protein ligases.",
RL J. Biol. Chem. 272:15085-15092(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 97264343.
RA Sutcliffe J.S., Jiang Y.-H., Galjaard R.-J., Matsura T., Fang P.,
RA Kubota T., Christian S.L., Bressler J., Cattanech B., Ledbetter D.H.,
RA Beaudet A.L.;
RT "The E6-Ap ubiquitin-protein ligase (UBE3A) gene is localized within
RT a narrowed Angelman syndrome critical region.";
RL Genome Res. 7:368-377(1997).
CC -i- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM
CC AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND
CC THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES.
CC -i- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -i- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.
CC -i- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
CC THIOESTER FORMATION.
CC -i- SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
CC DOMAIN.
CC -i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.
CC
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CC
DR EMBL; U96636; AAB6361.1; -
DR EMBL; U82122; AAB4756.1; -
DR MGD; MGI:105098; UBE3A.
DR INTERPRO; IPR000569; -
DR INTERPRO; IPR002106; -
DR PFM; PFM0632; HECT; 1.
DR PROSITE; PS50237; HECT; 1.
KW Nuclear protein; Ubiquitin conjugation; Ligase.
FT DOMAIN 405 410 ASP/GLU-RICH (ACIDIC).
FT BINDING 786 885 HECT.
FT CONFLICT 187 187 D -> E (IN REF. 2).
FT CONFLICT 301 301 L -> V (IN REF. 2).
FT CONFLICT 343 343 T -> S (IN REF. 2).
FT CONFLICT 384 384 N -> K (IN REF. 2).
FT CONFLICT 460 460 S -> F (IN REF. 2).
FT CONFLICT 486 486 G -> R (IN REF. 2).
FT CONFLICT 535 535 T -> R (IN REF. 2).
FT CONFLICT 577 577 DEGVGS -> MEKARP (IN REF. 2).
FT CONFLICT 584 584 E -> S (IN REF. 2).
FT CONFLICT 587 587 OL -> SM (IN REF. 2).
FT CONFLICT 597 597 D -> N (IN REF. 2).
FT CONFLICT 623 627 FTLLG -> VYSDWH (IN REF. 2).
FT CONFLICT 725 726 IS -> NL (IN REF. 2).
FT CONFLICT 817 817 L -> Q (IN REF. 2).
FT CONFLICT 869 870 NV -> KE (IN REF. 2).
SQ SEQUENCE 885 AA; 101175 MW; 55D885E080C6B699 CRC64;

Query Match 9.5%; Score 77; DB 1; Length 885;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 31; Conservative 20; Mismatches 35; Indels 30; Gaps 7;

DB 14 NINDOVLFVKRQVPE--DMTDIDQASQSPORLIIVYKSEVRGLAVLISYKSKS 71
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 402 NHNE-----DDEPIPESEELIQELGDERNNK-----KPRPRDLETLGK----- 446
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 447 TLDRKRLISFESEINERPLAVLEKNDYTF-----KVEIEN---KQSFVTC 491
| : : | : : | : : | : : | : : | : : | : : | : : | : : |

RESULT 13
ID Y809_METUA STANDARD; PRT; 167 AA.
AC 058219;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE HYPOTHETICAL PROTEIN MJ0809.
GN MJ0809.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Funtmann J.L., Nguyen D.,
RA Oltersback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -i- SIMILARITY: BELONGS TO THE M. JANNASCHII MJ0553 / MJ0809 / MJ1331 /
CC MJ1405 FAMILY.
CC
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CC
DR EMBL; U67525; AAB9881.1; -
DR TIGR; MJ0809; -
KW Hypothetical protein.
SQ SEQUENCE 167 AA; 19723 MW; DD998FE1329C0042 CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 167;
Best Local Similarity 26.8%; Pred. No. 2.3;
Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

DB 47 IIVYKDSVVRGLAVLISYKSK-----XSTLSCKNKIISFEEMP-----PENID 92
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 38 IIVYKDGTVRIILANDDDEDEKELFKYIERLEKKKDLIEIKERKRLNLYIEFPGIS 97
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 93 DIQSDLIFFOKRVPKMKKEFESELYEGHFLACQKEDDAFKLLKKEKNGDSVMEFTL 152
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 98 RLSSDDI-----LELNKKLIDEG-----VKYIKLIFALBEH--KKVLEIK 136
| : : | : : | : : | : : | : : | : : | : : | : : | : : |

DB 153 NLH 155
| : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 137 DMH 139

RESULT 14
HPPG_HELPY STANDARD; PRT; 621 AA.
AC P56116;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
DE HTPG OR HP0210.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

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CC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-26695 / ATCC 700392;
RX MEDLINE: 97394467.
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Loftus K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Lofthus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
CC
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CC -----
DR EMBL: AE000541; AAD07278.1; -.
DR HSSP: P07900; IYES.
DR TIGR: HP0210; -.
DR INTERPRO: IPR001404; -.
DR PFAM: PF00183; HSP90.1.
DR PRINTS: PR00775; HEATSHOCK90.
DR PROSITE: PS00298; HSP90.1.
KW Chaperone; ATP-binding; Heat shock.
SQ SEQUENCE 621 AA; 71274 MW; 28F198C1DC7EAB9A CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 621;
Best Local Similarity 23.2%; Pred. No. 11;
Matches 29; Conservative 27; Mismatches 52; Indels 17; Gaps 4;

QY 32 MTDIDOSASEPQRLIYYKSEVRGLAVTISVK---DSKASTYLSCKNKIISFEEMP 88
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 LRELVSNAADALDKLNYLMLTDEKLGNTPTPSIHLSFDSQKRTLTIKDNGMDKDLI 90
QY 89 ENIDDI-OSDLIFQKRVPGHNM-----EFESSLYEGHFLACQKEDDAFKLILKKDE 141
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 91 EHLGTAKSGTNTFLSALSGDKKDSALIGQFGVGFYSAFMYAS-----KIIVQTKKV 143

QY 142 NGDKS 146
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 NSDQA 148

RESULT 15
YK70_YEAST
ID YK70_YEAST STANDARD: PRT; 706 AA.
AC P36166;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HYPOTHETICAL 79.4 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.
GN YKR090W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Baladron V., Ballesta J.P.G., Bou G., del Rey F., Esteban P.F.,
RA Garcia-Cantalejo J.M., Garcia-Ramirez J.J., Gonzalez A., Jimenez A.,

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RA Revuelta J.L., Santos M.A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
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CC -----
DR EMBL: Z28315; CAA82169.1; -.
DR PIR: S38168; S38168.
DR SCD: S0001798; YKR090W.
DR INTERPRO: IPR001781; -.
DR PFAM: PF00412; LIM; 2.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS00478; LIM_DOMAIN_2; 2.
KW Hypothetical protein; LIM motif; Metal-binding; Zinc.
FT DOMAIN 536 612 LIM.
FT DOMAIN 621 672 LIM.
SQ SEQUENCE 706 AA; 79447 MW; B27DB9E09A39AA42 CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 706;
Best Local Similarity 22.2%; Pred. No. 13;
Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;

QY 9 TAVIRINDOYLFVDRKQPVFEDMTDIDOSASEPQ-----RLIYYKDESEVRGLAVTIS 64
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 428 TSIYQNSNTNL-----SKQTLIVDKGDVDEDAPESSITNGTPIFYKFKQSNVE-----YS 478
QY 65 VKDSKXSTLSCKNKIISFE--EMDPENIDIDSLIFQKRVPGH----- 108
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 479 NNEGMGSOEFPRYKLPTEALQOHKRNRTDLREE-IDNSKSDSHVLPNGGTTTRYSSDA 537
QY 109 -----NKKPEFESSLYEGHFLACQKEDDAFKLILKKDE 141
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 538 DYKETEPIEFKYPPEGPCRCAGLEVTKRRFRSKENE 575

Search completed: November 20, 2000, 14:07:54
Job time: 112 sec

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